

Entry name	O87490
Primary accession number	O87490
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 24, June 2003
Name and origin of the protein	
Protein name	RIBOSYLATING transferase ARR-2
Synonym	ADP-RIBOSYLATING transferase
Gene name	ARR-2 or ARR2
From	<u>Pseudomonas aeruginosa</u> [TaxID: <u>287</u>] <u>Escherichia coli</u> [TaxID: <u>562</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Pseudomonadales</u> ; <u>Pseudomonadaceae</u> ; <u>Pseudomonas</u> .
References	

- [1] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*P.aeruginosa*;
STRAIN=PATH2;
Tribuddharat C., Fennewald M.A.:
"Ceftazidime and rifampin resistance gene cassettes in an integron from *Pseudomonas aeruginosa*."
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*E.coli*;
TRANSPOSON=Tn2000;
MEDLINE=99169757;
Poirel L., Naas T., Guibert M., Chaibi E.B., Labia R., Nordmann P.:
"Molecular and biochemical characterization of VEB-1, a novel class A extended-spectrum beta-lactamase encoded by an *Escherichia coli* integron gene."
Antimicrob. Agents Chemother. 43:573-581(1999).
- [3] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*E.coli*;
TRANSPOSON=Tn2000;
MEDLINE=20566689; **PubMed**=11114922; [NCBI, ExPASy, EBI, Israel, Japan]
Naas T., Mikami Y., Imai T., Poirel L., Nordmann P.:
"Characterization of In53, a class 1 plasmid- and composite transposon-located integron of *Escherichia coli* which carries an unusual array of gene cassettes."
J. Bacteriol. 183:235-249(2001).

Comments

None

Cross-references

EMBL	AF078527; AAC64366.1; -. AF205943; AAG45718.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] [EMBL / GenBank / DDBJ] [CoDingSequence]
GO	GO:0046821; Cellular component: extrachromosomal DNA (inferred from electronic annotation). GO:0016740; Molecular function: transferase activity (inferred from electronic annotation).
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	O87490.
PRESAGE	O87490.
ModBase	O87490.
SMR	O87490; 20A38A8F35BE792C.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

KeywordsPlasmid; Transferase.**Features**

None

Sequence information

Length: 150 AA Molecular weight: 16940 Da CRC64: 20A38A8F35BE792C [This is a checksum on the sequence]

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      10      20      30      40      50      60
MVKDWIPISH DNYKQVQGPF YHGTKANLAI GDLLTTGFIS HFEDGRILKH IYFSALMEPA

      70      80      90     100     110     120
VWGAEIAMS LSGLEGRGYIY IVEPTGPFED DPNLTNKKFP GNPTQSYRTC EPLRIVGVVE

     130     140     150
DWEGHPVELI RGMLDSLEDL KRRGLHVIED

```

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Entry information

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Entry information

Entry name	O69275
Primary accession number	O69275
Secondary accession numbers	None
Entered in TrEMBL in	Release 07, August 1998
Sequence was last modified in	Release 07, August 1998
Annotations were last modified in	Release 26, March 2004
Name and origin of the protein	
Protein name	C2 toxin
Synonym	Component I
Gene name	None
From	Clostridium botulinum [TaxID: 1491]
Taxonomy	Bacteria ; Firmicutes ; Clostridia ; Clostridiales ; Clostridiaceae ; Clostridium .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=92-13;
[Hofmann F.](#), [Barth H.](#), [Aktories K.](#);
 "Clostridium botulinum DNA for C2 toxin (component-I), complete cds."
 Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AJ224480 ; CAA11969.1 ; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	Q46220 ; 1GIQ. [HSSP ENTRY / PDB]
GO	GO:0005576 ; Cellular component: extracellular (<i>inferred from electronic annotation</i>). GO:0009405 ; Biological process: pathogenesis (<i>inferred from electronic annotation</i>).
InterPro	IPR003540 ; Binary_toxinA.

Graphical view of domain structure.

Pfam

PF03496; Binary_toxA; 1.

Pfam graphical view of domain structure.

PRINTS

PR01390; BINARYTOXINA.

ProDom

[Domain structure / List of seq. sharing at least 1 domain]

HOBACGEN

[Family / Alignment / Tree]

ProtoMap

O69275.

PRESAGE

O69275.

ModBase

O69275.

SMR

O69275; 9CB348771CE038A8.

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UniRef

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Keywords

None

Features

None

Sequence information

Length: **431** Molecular weight: **49313** CRC64: **9CB348771CE038A8** [This is a checksum on the
AA **Da** sequence]

10	20	30	40	50	60
MPIIKEPIDF	INKPESEAKK	WGKEEEKRWF	TKLNNLEEEVA	VNQLKNKEYK	TKIDNFSTDI
70	80	90	100	110	120
LFSSLTAIEI	MKEDENHNLF	DVERIREALL	KNTLDRDAIG	YVNFTPKELG	INFSIRDVEL
130	140	150	160	170	180
NRDISDETLD	KVRQQIINQE	YTKFSFISLG	LNDNSINESV	PVIVKTRVPT	TFDYGVVNDK
190	200	210	220	230	240
ETVSLLLNQG	FSIIPESAI	TTIKGKDYIL	IEGSLSQELD	FYNKGSEAWG	AENYGDYISK
250	260	270	280	290	300
LSHEQLGALE	GYLHSDYKAI	NSYLRNNRVP	NNDELNKKIE	LISSALSVKP	IPQTLIAYRR
310	320	330	340	350	360
VDGIPFDLPS	DFSFDKKENG	EIIADKQKLN	EFIDKWTGKE	IENLSFSSTS	LKSTPSSFSK
370	380	390	400	410	420
SRFIFRLRLS	EGAIGAFIYG	FSGFQDEQEI	LLKNSTFKI	FRITPITSII	NRVTKMTQVV
430					
IDAEGIQNKE	I				

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Sequence analysis tools: [ProtParam](#), [ProtScale](#),
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Entry information

Entry name	O86171
Primary accession number	O86171
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 26, March 2004
Name and origin of the protein	
Protein name	C2 toxin
Synonym	Component-II
Gene name	None
From	Clostridium botulinum [TaxID: 1491]
Taxonomy	Bacteria ; Firmicutes ; Clostridia ; Clostridiales ; Clostridiaceae ; Clostridium .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=type C;
 MEDLINE=98323874; PubMed=9659689; [NCBI, ExPASy, EBI, Israel, Japan]
[Kimura K.](#), [Kubota T.](#), [Ohishi I.](#), [Isogai H.](#), [Isogai E.](#), [Fujii N.](#);
 "The gene for component-II of botulinum C2 toxin."
 Vet. Microbiol. 62:27-34(1998).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=type C;
 MEDLINE=96184657; PubMed=8645309; [NCBI, ExPASy, EBI, Israel, Japan]
[Fujii N.](#), [Kubota T.](#), [Shirakawa S.](#), [Kimura K.](#), [Ohishi I.](#), [Moriishi K.](#), [Isogai E.](#), [Isogai H.](#);
 "Characterization of component-I gene of botulinum C2 toxin and PCR detection of its gene in clostridial species."
[Biochem. Biophys. Res. Commun.](#) 220:353-359(1996).

Comments

None

Cross-references

EMBL D88982; BAA32537.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 HSSP P13423; 1ACC. [HSSP ENTRY / PDB]
 GO GO:0005576; Cellular component: extracellular (*inferred from electronic annotation*).
 GO GO:0009405; Biological process: pathogenesis (*inferred from electronic annotation*).
 InterPro IPR003896; Anthrax_toxinB.
 Pfam PF03495; Binary_toxB; 1.
 PRINTS PR01391; BINARYTOXINB.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 HOBACGEN [Family / Alignment / Tree]
 ProtoMap O86171.
 PRESAGE O86171.
 ModBase O86171.
 SMR O86171; 44C8153AC749D5F2.
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Keywords

None

Features

None

Sequence information

Length: **721** Molecular weight: **80515** CRC64: **44C8153AC749D5F2** [This is a checksum on the
 AA Da sequence]

10	20	30	40	50	60
MLVSKFENS	V KNSNKNYFTI	NGLMGYYFEN	DDFNLNIIISP	TLDGNLTF	SK EDINSILGNK
70	80	90	100	110	120
IIKSARWIGL	IKPSITGEYI	LSTNSPNCRV	ELNGEIFNLS	LNTSNTVNLI	QGNVYDIRIE
130	140	150	160	170	180
QLMSENQLLK	NYEGIKLYWE	TSDIIKEIIP	SEVLLKPNYS	NTNEKSKFIP	NNTLFSNAKL
190	200	210	220	230	240
KANANRDTDR	DGIPDEWEIN	GYTVMNQKAV	AWDDKFAANG	YKKYVSNP	FK PCTANDPYTD
250	260	270	280	290	300
FEKVSGQIDP	SVSMVARDPM	ISAYPIVGVQ	MERLVVSKSE	TITGDSTKSM	SKSTSHSSTN
310	320	330	340	350	360
INTVGAEVSG	SLQLAGGIFP	VFSMSASANY	SHTWQNTSTV	DDTTGESFSQ	GLSINTGESA

```

      370      380      390      400      410      420
      |       |       |       |       |       |
YINPNIRYYN TGTAPVYNVT PTTTIVIDKQ SVATIKGQES LIGDYLNPGG TYPIIGEPPM

      430      440      450      460      470      480
      |       |       |       |       |       |
ALNTMDQFSS RLIPINYNQL KSIDNGGTVM LSTSQFTGNF AKYNSNGNLV TDGNNWGPYL

      490      500      510      520      530      540
      |       |       |       |       |       |
GTIKSTTASL TLSFSGQTTQ VAVVAPNFSD PEDKTPKLTLEQALVKAFAL EKKNGKFYFH

      550      560      570      580      590      600
      |       |       |       |       |       |
GLEISKNEKI QVFLDSNTNN DFENQLKNTA DKDIMHCHIK RNMNILVKVI TFKENISSIN

      610      620      630      640      650      660
      |       |       |       |       |       |
IINDTNFGVQ SMTGLSNRSK GQDGIYRAAT TAFSFKSKEL KYPEGGRYMR FVIQSYEPFT

      670      680      690      700      710      720
      |       |       |       |       |       |
CNFKLFNNLI YSSSFDKGY DEFFYFYNG SKSFFNISCD IINSINRLSG VFLIELDKLI

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Entry information

Entry name **DTX_CORBE**
 Primary accession number **P00588**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 01, July 1986
 Sequence was last modified in Release 18, May 1991
 Annotations were last modified in Release 44, June 2004

Name and origin of the protein

Protein name **Diphtheria toxin [Precursor]**
 Synonyms **DT**
NAD(+)--diphthamide ADP-ribosyltransferase
EC 2.4.2.36
 Gene name None
 From Corynebacterium beta [TaxID: 10703]
 Taxonomy Viruses; dsDNA viruses, no RNA stage; Caudovirales;
Siphoviridae; Lambda-like viruses.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 MEDLINE=84070728; PubMed=6316330; [NCBI, ExPASy, EBI, Israel, Japan]
Greenfield L., Bjorn M.J., Horn G., Fong D., Buck G.A., Collier R.J., Kaplan D.A.;
 "Nucleotide sequence of the structural gene for diphtheria toxin carried by corynebacteriophage beta."
Proc. Natl. Acad. Sci. U.S.A. 80:6853-6857(1983).
- [2] SEQUENCE OF 33-225.
 MEDLINE=79194138; PubMed=221484; [NCBI, ExPASy, EBI, Israel, Japan]
Delange R.J., Williams L.C., Drazin R.E., Collier R.J.;
 "The amino acid sequence of fragment A, an enzymically active fragment of diphtheria toxin. III.
 The chymotryptic peptides, the peptides derived by cleavage at tryptophan residues, and the

- complete sequence of the protein.";
J. Biol. Chem. 254:5838-5842(1979).
- [3] ACTIVE SITE TRP-185.
MEDLINE=77134904; PubMed=849463; [NCBI, ExPASy, EBI, Israel, Japan]
Michel A., Dirkx J.;
"Occurrence of tryptophan in the enzymically active site of diphtheria toxin fragment A.";
Biochim. Biophys. Acta 491:286-295(1977).
- [4] ACTIVE SITE TYR-97.
MEDLINE=91115874; PubMed=1990001; [NCBI, ExPASy, EBI, Israel, Japan]
Papini E., Santucci A., Schiavo G., Domenighini M., Neri P., Rappuoli R., Montecucco C.;
"Tyrosine 65 is photolabeled by 8-azidoadenine and 8-azidoadenosine at the NAD binding site of diphtheria toxin.";
J. Biol. Chem. 266:2494-2498(1991).
- [5] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=92269934; PubMed=1589020; [NCBI, ExPASy, EBI, Israel, Japan]
Choe S., Bennett M.J., Fujii G., Curmi P.M.G., Kantardjieff K.A., Collier R.J., Eisenberg D.;
"The crystal structure of diphtheria toxin.";
Nature 357:216-222(1992).
- [6] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE=96155972; PubMed=8573568; [NCBI, ExPASy, EBI, Israel, Japan]
Bell C.E., Eisenberg D.;
"Crystal structure of diphtheria toxin bound to nicotinamide adenine dinucleotide.";
Biochemistry 35:1137-1149(1996).
- [7] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE=97164901; PubMed=9012663; [NCBI, ExPASy, EBI, Israel, Japan]
Bell C.E., Eisenberg D.;
"Crystal structure of nucleotide-free diphtheria toxin.";
Biochemistry 36:481-488(1997).
- [8] X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF COMPLEX WITH RECEPTOR.
MEDLINE=98324089; PubMed=9659904; [NCBI, ExPASy, EBI, Israel, Japan]
Louie G.V., Yang W., Bowman M.E., Choe S.;
"Crystal structure of the complex of diphtheria toxin with an extracellular fragment of its receptor.";
Mol. Cell 1:67-78(1997).

Comments

- **FUNCTION:** Diphtheria toxin, produced by a phage infecting corynebacterium diphtheriae, is a proenzyme that, after activation, catalyzes the covalent attachment of the ADP ribose moiety of NAD to elongation factor 2. Fragment A is responsible for enzymatic ADP-ribosylation of elongation factor 2, while fragment B is responsible for binding of toxin to cell receptors and entry of fragment A.
- **CATALYTIC ACTIVITY:** $\text{NAD}^+ + \text{peptide diphthamide} = \text{nicotinamide} + \text{peptide N-(ADP-D-ribose)diphthamide}$.
- **SUBUNIT:** Homodimer.

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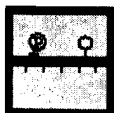
Cross-references

EMBL X00703; CAA25302.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

K01722; AAA32182.1; ALT_INIT.[EMBL / GenBank / DDBJ] [CoDingSequence]
 1DDT; 31-JUL-94. [ExPASy / RCSB / EBI]
 1MDT; 31-JUL-94. [ExPASy / RCSB / EBI]
 1DTP; 01-NOV-94. [ExPASy / RCSB / EBI]
 1TOX; 10-JUN-96. [ExPASy / RCSB / EBI]
 1SGK; 23-DEC-96. [ExPASy / RCSB / EBI]
 1XDT; 25-FEB-98. [ExPASy / RCSB / EBI]
 1F0L; 22-MAY-02. [ExPASy / RCSB / EBI]
 Detailed list of linked structures.
 InterPro IPR000512; Diphtheria_tox.
 Graphical view of domain structure.
 Pfam PF02763; Diphtheria_C; 1.
 PF01324; Diphtheria_R; 1.
 PF02764; Diphtheria_T; 1.
 Pfam graphical view of domain structure.
 PRINTS PR00769; DPTHRIATOXIN.
 ProDom PD025441; Diphtheria_tox; 1.
 [Domain structure / List of seq. sharing at least 1 domain]
 BLOCKS P00588.
 ProtoNet P00588.
 ProtoMap P00588.
 PRESAGE P00588.
 DIP P00588.
 ModBase P00588.
 SMR P00588; CAF82A75EA693FF8.
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Keywords

Toxin; Transferase; Glycosyltransferase; NAD; Signal; 3D-structure.

Features

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Key	From	To	Length	Description
SIGNAL	<u>1</u>	<u>32</u>	32	
CHAIN	<u>33</u>	<u>225</u>	193	Diphtheria toxin fragment A.
CHAIN	<u>226</u>	<u>567</u>	342	Diphtheria toxin fragment B.
ACT_SITE	<u>180</u>	<u>180</u>		
SITE	<u>185</u>	<u>185</u>	1	Modification inactivates enzyme.
BINDING	<u>53</u>	<u>53</u>		NAD.
BINDING	<u>97</u>	<u>97</u>		NAD.
DISULFID	<u>218</u>	<u>233</u>		
DISULFID	<u>493</u>	<u>503</u>		
CONFLICT	<u>178</u>	<u>180</u>		SVE -> VES (in Ref. 2).
HELIX	<u>34</u>	<u>36</u>	3	
TURN	<u>37</u>	<u>37</u>	1	

STRAND	<u>38</u>	<u>38</u>	1
HELIX	<u>40</u>	<u>42</u>	3
STRAND	<u>44</u>	<u>47</u>	4
TURN	<u>48</u>	<u>48</u>	1
STRAND	<u>50</u>	<u>55</u>	6
TURN	<u>57</u>	<u>58</u>	2
HELIX	<u>60</u>	<u>63</u>	4
TURN	<u>64</u>	<u>65</u>	2
TURN	<u>75</u>	<u>76</u>	2
HELIX	<u>80</u>	<u>82</u>	3
STRAND	<u>85</u>	<u>88</u>	4
HELIX	<u>91</u>	<u>95</u>	5
TURN	<u>96</u>	<u>97</u>	2
STRAND	<u>99</u>	<u>99</u>	1
TURN	<u>101</u>	<u>102</u>	2
TURN	<u>104</u>	<u>106</u>	3
STRAND	<u>109</u>	<u>109</u>	1
STRAND	<u>111</u>	<u>116</u>	6
STRAND	<u>120</u>	<u>126</u>	7
HELIX	<u>131</u>	<u>137</u>	7
TURN	<u>138</u>	<u>139</u>	2
HELIX	<u>146</u>	<u>150</u>	5
TURN	<u>151</u>	<u>151</u>	1
HELIX	<u>153</u>	<u>159</u>	7
TURN	<u>161</u>	<u>162</u>	2
STRAND	<u>165</u>	<u>171</u>	7
TURN	<u>174</u>	<u>175</u>	2
STRAND	<u>179</u>	<u>183</u>	5
TURN	<u>185</u>	<u>186</u>	2
HELIX	<u>187</u>	<u>190</u>	4
STRAND	<u>192</u>	<u>198</u>	7
TURN	<u>199</u>	<u>199</u>	1
HELIX	<u>200</u>	<u>202</u>	3
TURN	<u>206</u>	<u>207</u>	2
HELIX	<u>208</u>	<u>216</u>	9
TURN	<u>217</u>	<u>218</u>	2
HELIX	<u>238</u>	<u>254</u>	17
HELIX	<u>256</u>	<u>264</u>	9
HELIX	<u>272</u>	<u>286</u>	15
TURN	<u>287</u>	<u>288</u>	2
HELIX	<u>290</u>	<u>292</u>	3
HELIX	<u>293</u>	<u>299</u>	7
TURN	<u>300</u>	<u>301</u>	2
HELIX	<u>303</u>	<u>305</u>	3
HELIX	<u>307</u>	<u>320</u>	14
HELIX	<u>323</u>	<u>326</u>	4
TURN	<u>327</u>	<u>327</u>	1
HELIX	<u>329</u>	<u>336</u>	8

TURN	<u>337</u>	<u>338</u>	2
HELIX	<u>342</u>	<u>346</u>	5
TURN	<u>347</u>	<u>347</u>	1
STRAND	<u>348</u>	<u>349</u>	2
TURN	<u>350</u>	<u>351</u>	2
STRAND	<u>352</u>	<u>353</u>	2
HELIX	<u>358</u>	<u>375</u>	18
TURN	<u>376</u>	<u>378</u>	3
HELIX	<u>385</u>	<u>388</u>	4
TURN	<u>389</u>	<u>390</u>	2
HELIX	<u>391</u>	<u>407</u>	17
TURN	<u>408</u>	<u>408</u>	1
STRAND	<u>421</u>	<u>423</u>	3
TURN	<u>424</u>	<u>425</u>	2
STRAND	<u>426</u>	<u>430</u>	5
HELIX	<u>433</u>	<u>436</u>	4
STRAND	<u>437</u>	<u>439</u>	3
TURN	<u>440</u>	<u>441</u>	2
STRAND	<u>445</u>	<u>454</u>	10
STRAND	<u>459</u>	<u>461</u>	3
STRAND	<u>463</u>	<u>467</u>	5
STRAND	<u>469</u>	<u>469</u>	1
TURN	<u>470</u>	<u>472</u>	3
STRAND	<u>473</u>	<u>475</u>	3
TURN	<u>477</u>	<u>479</u>	3
STRAND	<u>481</u>	<u>484</u>	4
TURN	<u>485</u>	<u>486</u>	2
STRAND	<u>487</u>	<u>496</u>	10
TURN	<u>497</u>	<u>499</u>	3
STRAND	<u>500</u>	<u>505</u>	6
STRAND	<u>509</u>	<u>512</u>	4
TURN	<u>513</u>	<u>514</u>	2
STRAND	<u>515</u>	<u>515</u>	1
STRAND	<u>517</u>	<u>525</u>	9
TURN	<u>533</u>	<u>534</u>	2
STRAND	<u>540</u>	<u>550</u>	11
TURN	<u>551</u>	<u>552</u>	2
STRAND	<u>553</u>	<u>562</u>	10
STRAND	<u>564</u>	<u>567</u>	4

Sequence information

Length: **567 AA** [This is the length of the unprocessed precursor]

Molecular weight: **61601 Da** [This is the MW of the unprocessed precursor]

CRC64: **CAF82A75EA693FF8** [This is a checksum on the sequence]

10	20	30	40	50	60
MLVRGYVVSR	KLFASILIGA	LLGIGAPPSA	HAGADDVVDS	SKSFVMENFS	SYHGTPGYV
70	80	90	100	110	120

```

DSIQKGIQKP KSGTQGNYYD DWKGFYSTDN KYDAAGYSVD NENPLSGKAG GVVKVITYPGL
      130      140      150      160      170      180
      |      |      |      |      |      |
TKVLALKVDN AETIKKELGL SLTEPLMEQV GTEEFIKRFG DGASRVVLSL PFAEGSSSVE
      190      200      210      220      230      240
      |      |      |      |      |      |
YINNWEQAKA LSVELEINFE TRGKRQDAM YEYMAQACAG NRVRRSVGSS LSCINLDWDV
      250      260      270      280      290      300
      |      |      |      |      |      |
IRDKTKTKIE SLKEHGPIKN KMSSEPNKTV SEEKAKQYLE EFHQTALEHP ELSELKTVTG
      310      320      330      340      350      360
      |      |      |      |      |      |
TNPVFAGANY AAWAVNVAQV IDSETADNLE KTTAALSILP GIGSVMGIAD GAVHHNTEEI
      370      380      390      400      410      420
      |      |      |      |      |      |
VAQSIALSSL MVAQAIPLVG ELVDIGFAAY NFVESIINLF QVVHNSYNRP AYSPGHKTQP
      430      440      450      460      470      480
      |      |      |      |      |      |
FLHDGYAVSW NTVEDSIIRT GFQGESGHD I KITAENTPLP IAGVLLPTIP GKLDVNKSKT
      490      500      510      520      530      540
      |      |      |      |      |      |
HISVNGRKIR MRCRAIDGDV TFCRPKSPVY VGNGVHANLH VAFHRSSEK IHSNEISSDS
      550      560
      |      |
IGVLGYQKTV DHTKVNSKLS LFFEIKS

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